

SEQUENCE LISTING



(1) GENERAL INFORMATION:

(i) APPLICANT: Ishiwata, Tetsuyoshi; Sakurada, Miki; Nishimura, Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada, Shigemasa; Takei, Masami

(ii) TITLE OF INVENTION: IgA Nephropathy-Related Genes

(iii) NUMBER OF SEQUENCES: 111

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto

(B) STREET: 30 Rockefeller Plaza

(C) CITY: New York

(D) STATE: New York

(E) ZIP: 10112-3801

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

(B) COMPUTER: Compac PC

(C) OPERATING SYSTEM: Windows 95

(D) SOFTWARE: WordPerfect 8.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/090,672

(B) FILING DATE: 04-JUNE-1998

(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/JP97/04468

(B) FILING DATE: 05-DEC-1997

(A) APPLICATION NUMBER: JP-8-325763

(B) FILING DATE: 05-DEC-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Perry, Lawrence S.

(B) REGISTRATION NUMBER: 31865

(C) REFERENCE/DOCKET NUMBER: 766.21

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 218-2100

(B) TELEFAX: (212) 218-2200

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4276 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTCTACCGTT TTTCCCTGC TTTCTATTCC AGGTCAGTCT TCACTGTTTC CG ATG GAA	58
Met Glu	
1	
GAT GGA TTC TTG GAT GAT GGC CGT GGG GAT CAG CCT CTT CAT AGT GGC	106
Asp Gly Phe Leu Asp Asp Gly Arg Gly Asp Gln Pro Leu His Ser Gly	
5 10 15	
CTG GGT TCA CCT CAC TGC TTC AGT CAC CAG AAT GGG GAG AGA GTG GAA	154
Leu Gly Ser Pro His Cys Phe Ser His Gln Asn Gly Glu Arg Val Glu	

20	25	30	
CGA TAT TCT CGA AAG GTG TTT GTA GGC GGA TTG CCT CCA GAC ATT GAT			202
Arg Tyr Ser Arg Lys Val Phe Val Gly Gly Leu Pro Pro Asp Ile Asp			
35	40	45	50
GAA GAT GAG ATC ACA GCT AGT TTT CGT CGC TTT GGC CCT CTG ATT GTG			250
Glu Asp Glu Ile Thr Ala Ser Phe Arg Arg Phe Gly Pro Leu Ile Val			
55	60	65	
GAT TGG CCT CAT AAA GCT GAG AGC AAA TCC TAT TTT CCT CCT AAA GGC			298
Asp Trp Pro His Lys Ala Glu Ser Lys Ser Tyr Phe Pro Pro Lys Gly			
70	75	80	
TAT GCA TTC CTG CTG TTT CAA GAT GAA AGC TCT GTG CAG GCT CTC ATT			346
Tyr Ala Phe Leu Leu Phe Gln Asp Glu Ser Ser Val Gln Ala Leu Ile			
85	90	95	
GAT GCA TGC ATT GAA GAA GAT GGA AAA CTC TAC CTT TGT GTA TCA AGT			394
Asp Ala Cys Ile Glu Glu Asp Gly Lys Leu Tyr Leu Cys Val Ser Ser			
100	105	110	
CCC ACT ATC AAG GAT AAG CCA GTC CAG ATT CGG CCT TGG AAT CTC AGT			442
Pro Thr Ile Lys Asp Lys Pro Val Gln Ile Arg Pro Trp Asn Leu Ser			
115	120	125	130
GAC AGT GAC TTT GTG ATG GAT GGT TCA CAG CCA CTT GAC CCA CGA AAA			490
Asp Ser Asp Phe Val Met Asp Gly Ser Gln Pro Leu Asp Pro Arg Lys			
135	140	145	
ACT ATA TTT GTT GGT GGT GTT CCT CGA CCA TTA CGA GCT GTG GAG CTT			538
Thr Ile Phe Val Gly Gly Val Pro Arg Pro Leu Arg Ala Val Glu Leu			
150	155	160	
GCG ATG GTA ATG GAT CGG CTA TAC GGA GGT GTG TGC TAC GCT GGG ATT			586
Ala Met Val Met Asp Arg Leu Tyr Gly Gly Val Cys Tyr Ala Gly Ile			
165	170	175	
GAT ACC GAC CCT GAG CTA AAA TAC CCA AAA GGA GCT GGG AGA GTT GCG			634
Asp Thr Asp Pro Glu Leu Lys Tyr Pro Lys Gly Ala Gly Arg Val Ala			
180	185	190	
TTC TCT AAT CAA CAG AGT TAC ATA GCT GCT ATC AGT GCC CGC TTT GTT			682
Phe Ser Asn Gln Gln Ser Tyr Ile Ala Ala Ile Ser Ala Arg Phe Val			
195	200	205	210
CAG CTG CAG CAT GGA GAG ATA GAT AAA CGG GTA AGC CTT ATA CTA CAT			730
Gln Leu Gln His Gly Glu Ile Asp Lys Arg Val Ser Leu Ile Leu His			
215	220	225	
TTT GGA AAA TTC TAGAAATGGT CCTCTAAATG TGTGATTACC AATATTAGAA			782
Phe Gly Lys Phe			
230			
CGGGAGCATT TTATGACAAT AAAGTGACAG CTGACAATTT TGCCTATAGA GTTAATTATG			842
GTCTATAATA CATGAAATAA TGTCCTATGA ATTTCTTTTA TCTTTCAGTT TTTTGAGTAG			902
CCTAATCAGA ACACTACAAT TTA CTGAGT TAATTTAATC TTCTCTAACT TCCATTCAAT			962
CTCAATCCAT CCGTCCATTC ATTCACCTAG TTTGTAAGTC ATTCAATAAA TATTTACTGA			1022
ATCCTTTGTT CTGTGTTATA TCAAGTATAC AAACAGGAAT GCCCTTGAGG TTTCTGCCC			1082
TTTTTTTTGT TTGTTTTTTA ATCCTGGGAC ATAGGGAAGA CCTCAGCAAG CCCTATTTCT			1142
CAATGAATTG TACTCACAGA TTTCTTTTTT TTTTTTTTTT TCTTTTTCCA CAGCCGCCAC			1202
CTCTCACCGA TTTATTCCTT AGCTTGGTGT TTCATGTATT CAACAAACGT TTAGTGCTT			1262
AGGGCAAGAA GTTCCTGTCC TCATGAGTTT ATTTCTTAGC AGATAGAACT GTATCACTTG			1322
CCAGTACTAG TCAGAGTGTG GCCTGTGGAC TGACCTCCAG TCTGTAACT TAGTTGTAG			1382
TGAGATAGCA ATTTAGACCA GAATGTGTAA TCAACCACAT TACTGGGCAC AATGTTTGGT			1442
CCAGCTGGCG ATTTTTTTT CATAGAAAGC CTTTATTGAT GAGGGAAGCA ATATATTGAT			1502
TTATATTTTG GGGTCACCTT TTTATTTTCAT GGCACACTGG CACTTTCATG CATGCTGACT			1562
TTGATATCCA TCACTCTGAG GCATTGTGCT AAAATAGATT GATTTTATCG TGTGTTCTC			1622
AATCAAGAT GTAAAAATCA TCAAGTCAGT AGCAGTTTTT GCTTTTTATG TTTTCATGTA			1682

TGTACAGTCT	ACTTCACTGG	CAGTAAAAAA	ATTTAAGATA	GTGGTGGTCA	TCCTACAAAC	1742
TGTGAATCTA	TTAAAGAGAA	AAGTATCTGT	TCTATTCTAA	GCATGGGGGA	GGGACAAGAT	1802
TAGTATGTTA	ACATGCCTAC	TTTGTTTGTT	TGAGATGGAG	TCTCTCTCCG	TCACCCAGGC	1862
TGGAGTGCAG	TGGTACAGTC	TCAGCTCACT	CCAACCTCTG	CCTCCCGGGT	TCAAGTGATT	1922
CTCCTGCCCT	AGCCTCCCGA	GTAGGTGGAA	TTACAGGCAT	ATACCACCAT	GCCCAACAAA	1982
TGTTTGTATT	TTTAGTGGAG	ACAGGGTTTC	ACCGTGTTGG	TCAGGCCAGT	TTCAAATCC	2042
TGACCTCAAG	GGATCCACCT	GCCTCACCCC	CTCAAAGTGC	TGGGATTACA	GGCATGAGCC	2102
ACCCACCATG	CCTGGCCTAC	TTGGTTTTTT	ATGCACACTA	AAAAATACCT	ACATCTCACT	2162
GCCTTATTCC	AACATAAGTT	TCAGAGCTGT	GGGATTGGTC	ATTAGAAATT	CAGACTGAAT	2222
TTGTGTTCCCT	CTGCAATGAA	ATCCTTTGCC	CAGTGTTCAT	GTCACTCTGT	AGACATTATG	2282
GAGCAGCCTA	GAGGCCAGAA	GCCCAGTGCT	CTCCTTATGC	CTGCTCTTCC	TGGGCTTCGT	2342
GACACTCTTC	TTCTCCTTTT	GTACTTTTAT	TTTTTTAGTT	AAAAAATTTT	TTTTAGAGGG	2402
AGGGTCTCAC	TCTGTCACCC	AGGCTGGAGC	ACAGAATCAC	AATCATGACT	CACTGCATGT	2462
TCTTCTCCTT	TTGTTTATGG	CTAATCTTGG	TCAGGATTCC	TTGTCAGAGC	TGGGTGGCAC	2522
CAGTGCTGGT	GACAGCCTGC	TGTAAGGGAG	TTTCAGCCAT	GAATCTCTCC	AGACTAAAAA	2582
TAACCAGCTC	TTTTCTAGCT	GATGAATTAA	TAACCAGGTG	ACTGTTAATG	CTTGAAAGGT	2642
TCACATGACA	GGTTGGCCGA	TAGAACGCTG	GAACAGGCCC	AGTTTTAGAA	ATTACCTCT	2702
GACTTTTAGA	CTCAGGTGAA	CCATTCTTAC	TGAGAAAGAA	CAAAGCAGGG	TTTTTAGACTG	2762
TGAATCCCTAT	GGCTGCATCT	TTTTTTTTTT	TTTAACAGAG	TTCCAGGTTT	GTGATTATAA	2822
CCCAACATGT	GTACACTATA	AATAGAAACC	ACGAGCCAGG	CTTTTTACGA	CAGCTCAGAA	2882
TCTTGTGACG	CAGTAGTCAG	GCATCTTCAC	ACCGACTTGA	ATATTGAAGT	GCAGTTGTGT	2942
GGAACCTGGA	TCATCTTAGT	TGATTTTGTT	TAAATTATGA	TTCCACATAT	GACAAAAATC	3002
CAGATCCACT	AATTAATAATG	AGGGTTTATG	TCTATGAATA	ATCTCCTGTG	GGTTTAACTC	3062
CATAACATTC	TAGTCTAAAC	AGTTGGCTTC	ACTTCATGAT	GTCTGCTCAA	ATCCTTTTTC	3122
CTTTAAAGGA	TGTTTATTTA	ATAAGAAAAA	AAATGTAAAA	TGATAGATAA	TAAAGCCTT	3182
ACTAGTTTCT	TAAAAGATGA	ACTATCCATA	TTTCAGTAAA	TGAATAATTA	GTCTTCCCTC	3242
TTTGGGCACC	TTGGAACAGA	TTCATTGAGA	TAGTGGGTGG	AAATGTACAT	GTATGGTAAG	3302
CATTGCTGGC	CTAGTCACTG	AAAAATGTAA	ACTCTTATTT	TTGATTGCAG	GTGGAAGTTA	3362
AGCCATATGT	CTTGATGAT	CAGCTGTGTG	ATGAATGTCA	GGGGGCCCGT	TGTGGGGGGA	3422
AATTTGCTCC	ATTTTTCTGT	GCTAATGTTA	CCTGTCTGCA	GTATTACTGT	GAATATTGCT	3482
GGGCTGCTAT	CCATTCTCGT	GCTGGCAGGG	AATTCCACAA	GCCCCCTGGT	AAGGAAGGCG	3542
GTGACCGCCC	TCGGCATATT	TCATTCCGCT	GGAACATAAG	GATAACTGCA	GTGCTCATTT	3602
TCAGGCCTCA	GAATAAGTGC	ACTCTTCTGT	TCATTCTGAC	CCCTTCTCTA	ACCTCTTCAC	3662
GCTGGCATGT	CCTTTTGTAG	CAGTCTGTAA	CTTAACATA	GTATAATGAA	AAGAATGACC	3722
TATAATATAG	GTGTTTTGTA	GATTCTTGTG	TCAGTCAAAA	CAATATGAAC	TCCTTTTTTCG	3782
TATTGCCATC	GGGTTGCATG	GAAGTTTTAT	TCTCTTGTTT	TGCTGGAAAC	CAAGAGGATC	3842
CAAACCTTCCT	GCAACATTTT	CTTAGAGGAG	AGAGAGAAAT	ATTAAGAGAG	AAATGAAACA	3902
ATAGAGTATT	TTGGGTTTTT	AATTAAATTA	TTGTTAATAA	TATAACATAT	AAGAATACTT	3962
TTATTAAAAA	AACCATGCAA	CAATAACACT	ATCGGTCTAT	CTGACAGTTT	TTCCCCCAGG	4022
GAAGTGCTTT	TGCCTTTTCC	TTTCTTTTTT	TTTTTTTTTC	ATCTTTTTTG	TTCTCTCTCT	4082
TTTTTCCATC	CCTTTTTAAT	TTTTTTAACA	GCAATGGAGG	AAGTTAACAA	TTTTTAATGG	4142
AAAGAGCATG	TTAGAGCAAA	CAAATGCATA	AGCAAGACTG	AGCAGCATTA	TAATTAATTT	4202
TCAGGGTTTT	GAGGCTGAAC	ATAATTTTAT	TATCCCTCAA	AAAGTTACCA	CCACATCAGA	4262
AAAAAAAAAA	AAAA					4276

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: l ukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTTGGAGGTT CTGGGGCGCA GAACCGCTAC TGCTGCTTCG GTCTCTCCTT GGGAAAAAAT	60
AAAATTTGAA CCTTTTGGAG CTGTGTGCTA AATCTTCAGT GGGACA ATG GGT TCA	115
Met Gly Ser	
1	
GAC AAA AGA GTG AGT AGA ACA GAG CGT AGT GGA AGA TAC GGT TCC ATC	163
Asp Lys Arg Val Ser Arg Thr Glu Arg Ser Gly Arg Tyr Gly Ser Ile	
5 10 15	
ATA GAC AGG GAT GAC CGT GAT GAG CGT GAA TCC CGA AGC AGG CGG AGG	211
Ile Asp Arg Asp Asp Arg Asp Glu Arg Glu Ser Arg Ser Arg Arg Arg	
20 25 30 35	
GAC TCA GAT TAC AAA AGA TCT AGT GAT GAT CGG AGG GGT GAT AGA TAT	259
Asp Ser Asp Tyr Lys Arg Ser Ser Asp Asp Arg Arg Gly Asp Arg Tyr	
40 45 50	
GAT GAC TAC CGA GAC TAT GAC AGT CCA GAG AGA GAG CGT GAA AGA AGG	307
Asp Asp Tyr Arg Asp Tyr Asp Ser Pro Glu Arg Glu Arg Glu Arg Arg	
55 60 65	
AAC AGT GAC CGA TCC GAA GAT GGC TAC CAT TCA GAT GGT GAC TAT GGT	355
Asn Ser Asp Arg Ser Glu Asp Gly Tyr His Ser Asp Gly Asp Tyr Gly	
70 75 80	
GAG CAC GAC TAT AGG CAT GAC ATC AGT GAC GAG AGG GAG AGC AAG ACC	403
Glu His Asp Tyr Arg His Asp Ile Ser Asp Glu Arg Glu Ser Lys Thr	
85 90 95	
ATC ATG CTG CGC GGC CTT CCC ATC ACC ATC ACA GAG AGC GAT ATT CGA	451
Ile Met Leu Arg Gly Leu Pro Ile Thr Ile Thr Glu Ser Asp Ile Arg	
100 105 110 115	
GAA ATG ATG GAG TCC TTC GAA GGC CCT CAG CCT GCG GAT GTG AGG CTG	499
Glu Met Met Glu Ser Phe Glu Gly Pro Gln Pro Ala Asp Val Arg Leu	
120 125 130	
ATG AAG AGG AAA ACA GGT GAG AGC TTG CTT AGT TCC TGATATTATT	545
Met Lys Arg Lys Thr Gly Glu Ser Leu Leu Ser Ser	
135 140	
GTTCTCTTCC CCATTCCCAC CTCAGTCCCT AAAGAACATC CTGATTCCCC CAGTCTTCAA	605
GCACATGAAT TCAGAATGAA AGGTTTGCCA TGGCTAAGGA ATGTGACTCT TTGAAAACCA	665
TGTTAGCATC TGAGGAACCT TTTTAAACTT TGTTTTAGGG ACTTTTTTTT CCTTAGGTAA	725
GTAATGATTT ATAAACTCCT TTTTTTTTTT TTGACTATAG TCGGTTGCAT GGTTACTTTA	785
AGCGTGGAAT CAAATGGAGT GGCATTTAGT TCAGGCGGCT TGTTCCCTTG CATTGGCAAAG	845
TATCAAGAAG ATCCCCAAGT CAAGTCACAT TTGTAAAGCT GCTTCCCAAT TGGCTTTGTC	905
ACGCACTGTT GAAGCAGTGG GAGAGAGATT CACCTGTTAT AAAGGAACTG ACTAACACAA	965
GTATCCCGTC TATATCTGAA TGCTGTCTCT AGGTGTAAGC CGTGGTTTCG CCTTCGTGGA	1025
GTTTTATCAC TTGCAAGATG CTACCAGCTG GATGGAAGCC AATCAGGTTG CTTCACTCAC	1085
CAAGTCTAGA TATTCATGAA AATGGAACAA GTCTGTACAA TTTTAAAAAA AGGTTGAAGG	1145
AGTGGTTTGT TCCAAAGGAG TGACTTTTTT TTAATAAAAAA AAGCTTTGTA TATATTAAAA	1205
TTGATGTTAC TAGAATAAGT ACAGTACCAA GGACTTCATT ATAGAATTTG TTCTGCCTTT	1265
AAACATGGCT ACCTACCTGG CAGGGCTTTG TTAACACTG AATACCTGTC TGGTAATCAC	1325
TAAACATCT TAATGTTTCC CTTTTTTCTA GTTTGTTATA TTCCTATTAT GTCCATTGAG	1385
AGTAAGCTTA GTATATCAA CTCTCCATTT GACAGTGAAG AGAACATAGT GAAAGTCTGT	1445
GGCGGCATTT TTATAAGTAA TTCCTTATTT CTGCCTGAAG ACCACAAAGC CTCCTGGAGG	1505
CGTAAGTCTG GAGATTAGCC TGGGAGTGGT GTCCTGCAGC TGTCTAATCT AGTTAGAGTG	1565
TAAGTCTGAT GAGATTAGCC TGGGAGTGGT GTCCTGCAGC TGTCTAATCT AGTTAGAGTG	1625
GCATTAACAT TCTAATCTCC TTGAGAATGC CTTTTATAGT CTGTTCAAAG CAAGTCATTG	1685
ATGGTTCCTC GAGGTAGTGT TAACTGAAGT GTTCTTCAGT TTGTCAAGAT AATGTTCAAGT	1745
GCTTGGCACT TAAATAACAT TTTTTCGAAG AACTCCAAGG CACATTATTG AATGCCTTTA	1805
ACCAAGTGCA TTCTGGGAAG TTTGCTTGAC TCATTATCTT GCTTTTCTGC AGCATTCTGT	1865
GATTTGAGTC ATCCATGAAT CCATGAATAA AAGTTACATT CTTTGATTGG TAATATTGCC	1925

ATTTATAACA	AGACTCACTA	ATGAGGGTAT	CACTTTGACT	GACTGATTG	TTAAAGTTTT	1985
TAAGCCTCTC	ATTTTCCTAA	CCCAGAAATC	ACAGCCTGAT	TTTATTAAAA	GTAGAGCTTC	2045
ATTCATTTCA	TACCATAGAT	ACCATCCTAG	TAAATCCAGA	ACATATACAA	GGTTCATGTG	2105
AGTCTGCTTT	CTTGACATGA	TAGCATTGTT	TGATGCAGTG	GATATGTCAG	AATGACTAAC	2165
CTAGGAGTTT	AAAACCTCCTA	AGAAACTAAA	ACCTGTAAGA	CATTTAAAAG	TCTCCACAAT	2225
TTTAATGTAT	ACAAAGCTAT	GTTACTGTGT	AACACATTAC	AGTTCAAATT	CACTCCAGAA	2285
ATAAAAGGCC	AGTAGGATTA	GGGACTCACT	GGTAGTTTGG	AGTCTCCCAG	CACACATCCC	2345
TCCTAGTGGG	ATGATCTATT	CACATATCTC	CCAGCTTTTT	TATTTTGTGCT	TCTGTATATC	2405
ACAGTGAGTG	GATGGCCCTT	CAGCTTTTTT	TCTCCTGGCC	AGACATGCAG	TCTTGCCTTT	2465
AGATATCGCA	GAGACAAAAT	TCACAGCATG	TCTTAAATCT	TCCAGGATTT	GCAAGAACCA	2525
AATTGCTCAA	CAGTATGTAT	GTTTAGAGGG	GTTAGACTCC	TTTTTAAAAT	CTGGATATCT	2585
AACCACCTAC	TTAAATCTGT	TTGATAGTGT	CAAACCACCC	CCACCCTTGA	TCCTCCCACC	2645
CCCCAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAA		2689

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCTCTCTCTC	TCTTTCACAG	AGTCTTGCTC	TGTCGCCAG	GCTGGAGTGC	AGTGGCACAA	60
TCTCACTGCA	AGCTCCGCCT	CCTGGGTTCA	CGCCATTCTC	CTGCCTCAGC	CTCCCAAATA	120
GCTGGGACAA	CAGGCACCTG	CCACCACGCC	CGGCTAATTT	TTTGATTTT	TAGTAGAGAC	180
AGGGTTTCAC	CATGTTAGCC	AGGATGGTCT	CAATCTCCTG	ACCTCGTGAT	CCACCCGCCT	240
CAGCCTCCCA	AAGTGCTGAG	ATTACAGGTG	TGAGCCACCA	CGCCCAGCCA	CATCTTTCTT	300
TCTTTCTTTT	TGGTTTTTGT	TTGTTGTTTG	AGACAGGGTC	TTGCTCTGTC	GCCCTGGCTC	360
ACGTGAACCT	CCCACCTCAG	CCTCCCAAGT	AGCTGAGACC	ACAGGTGTGA	GCCACCACTC	420
CTGGGTAAATG	TTTGATTTT	TTGTAGAGA	TGGGGTTTCA	CCGTGCTGCC	CAGACTGCTC	480
TCAAACCTCT	GGGCTCAAGT	GATCCACCTG	CCTTGACCTC	CTAAAGTGCT	GGAATTACAG	540
GTGTGAGCCA	CCGTGCTCAG	CCGAGTGTCT	TTCGTATGTT	TTCTGAGCAC	GTGGATTTC	600
ATCTCTCTGC	ATTCTCTGTT	CATCTCAGCC	TGTTTGTTCC	ATTGAGATAA	ATGACTTTTT	660
CTTGGTAACT	TAGAGTACTT	TGTGTATTTA	CAGGTTAATC	CCTTATCAAT	TTATATCAGT	720
TGCTGCTATC	TTTTCTTAGA	TTTTTCTTTT	CATTTTAAAA	ATTACATTGT	TTCAATGAAC	780
AGAATTTTTTA	AGTTTTTAACG	TAGTCCACTT	TGTCCATTTT	CTTTATGACC	GGTGCATTTT	840
AGGGTCTTGT	TTAAGAAATC	GTTCTTTATC	CTGAGGTCAT	AAAGATAGTC	TACTGTATTT	900
TCTTTTAAGA	GCTGAAAAGG	TGTTTTATAT	TTAATTTATT	TGGGATTGGC	TTTTGTGTGG	960
TGGGGATAAG	GATCACAAAT	TTATTTCAAT	TTTTTTCCAC	TTGGTTATGC	CAGTGGCCCC	1020
ATTTCCATTT	TTTGAATAGT	CTTCTGTGTC	AGAAAAGACT	TCACTAGCAG	AGAAGTCCTG	1080
AGACTTACCC	TTCAAAAGGC	CCCATTCACA	AGGCTAGCAC	TTGGCGTGCA	TCTGAGAACC	1140
TGGATTTTGG	GGTGGTTCCT	ATAATGTGGT	GTATGCTGAA	CACCCACCTT	TCCTTCTGGG	1200
AGTCTGGAAT	TTGGGTATAT	GTTGGACAGA	GGCTGCCTAA	GTGACCAGCT	TCAACAACAG	1260
CCCTGGGTGC	TGGGTCACCTC	ATGACCCATA	GACAAA ATG	CCA CAC ATG	TTG TCA	1314
			Met	Pro His Met Leu Ser		
			1	5		
CAG CTT ATT GCT GGA GGA GTT AGC ACA TCC TGT	GTG ACT GCA CTG GGA					1362
Gln Leu Ile Ala Gly Gly Val Ser Thr Ser Cys	Val Thr Ala Leu Gly					
10	15	20				
GAG GAA ACT GGT GCC TGG TTC CCT GTG TAT TTG	TCC CAC GCC TCC AGT					1410
Glu Glu Thr Gly Ala Trp Phe Pro Val Tyr Leu	Ser His Ala Ser Ser					
25	30	35				

CCC TTT GCT GAT CTC GTT TTT TGT CCT TTT GCT GAG ATA AAT CAC AGC	1458
Pro Phe Ala Asp Leu Val Phe Cys Pro Phe Ala Glu Ile Asn His Ser	
40 45 50	
CAG GAG TAT GAC AAT ATG CGG GGT CCT GTG AGT CCT CCT AAC AAA CAG	1506
Gln Glu Tyr Asp Asn Met Arg Gly Pro Val Ser Pro Pro Asn Lys Gln	
55 60 65 70	
TTC AAT CTG GGG GTG ATC TTT GGG ATC CCC AAC AAC TGT CGT TTC CCC	1554
Phe Asn Leu Gly Val Ile Phe Gly Ile Pro Asn Asn Cys Arg Phe Pro	
75 80 85	
ACT GAT AAT AAA ATA ACT GAG AAG CAG CTA TTG GGC AAT GTT CTG AAC	1602
Thr Asp Asn Lys Ile Thr Glu Lys Gln Leu Leu Gly Asn Val Leu Asn	
90 95 100	
TAC CCT TGAACATTCA TGTCTTCATC TGAACATCCA TCTACTACCC CTGATTTTTT	1658
Tyr Pro	
104	
CAGTGCAGGG TGCATATCCT GTATCACCCA ATAAATGGTC ATTGATCACC ATAGGAAAGG	1718
AACAGTGAAG GCTCCACGGT GGTTTGGAGG AAGGTGGCAG GCATTTCAGCG GTAACTTTTT	1778
TGAGCAGATA GATTTTATGT TTTTGCAATG AGTGAAATAA ATTTTCCCAT ATCTATTTAA	1838
GGTTGGCAAT CATTATCTTT TTATCATCTT GGAACATTG GAATTCCTTT AATATGTTTA	1898
GTTAGGAATT TTCTACCTTC CTCATCTTGT CCGATAGTTT AAAATCCAC AGTTATTTCA	1958
CGGGCTCCTC ATACCTGCCT GTGTGATTTC TAACATGTCA CGCTATGCAA CCAGTTGCTT	2018
TTACTTGTAG AGTGTTCCTT TAGGTAATAG CTTATTATTG GTTATGTGAT TACAGTGTGT	2078
TAAAGACAGG TCTGTAGTTA TGTAAAATGC CGTTTCTCTG AGTATCATGG TCATTTCCAC	2138
ATATTTCTCT ATTCATGTAT TTGTAAGAAT ATATCTATT TTGCAGTATT TTATTTATTT	2198
ATTTTATTTT ATTTTCTGAA ACGGAGCCTT GTTCTGTCTC CTAGGCTGGA GTGCAGTGGT	2258
GTGATCTCGA CTCACTGTGA CCTCCCCCTC CCAGGTTCAA GCGATTCTCC CGCCTCATCC	2318
TCCCAAGTCA TTGGGATTAC AGTCACGTGC CATGAAGCCC TGCTAATTTT TTGTATTTT	2378
AGTAGAGACA GGATTTCAAC ATGTTGGCGA TGCTGGTTTC GAACTCCTGG TTTGAACTC	2438
CTGACCTCAA GTGATCCACC TGCCTCGGCC TCCCAAAGAA CTGGGATTAT GGGCGTGAAC	2498
CACCACGCCA GGTCAGTTTT GCAGTGTTTT AAATACTGTT GTCTTTGAGA GGAGAGAGGC	2558
ACGCACATAG ACTATGGTGA TTACCATCAT ATACTGGAAA GTGCAAAGTG TAGCGCAGTT	2618
AACGTGTGAGC CATCTCATCA AACCCTAACA GATGTCTCAT TTGTCCATAA AGGGGCTTCT	2678
GTCCCATAGA AATTCATGTA CCCAACCTAC TCTTCAACCA TGATTTTTCT CTGATGGCCT	2738
GTGTGAACAG ATTAATGGTG TCCATCTAAT TCCTTCCCCA CTGGGGGAAA GCAAATCATC	2798
AGGCCCATTG CAAAACTGC TCTTGGTTGA GCTTCCTGCC TTAAATCATA CCCACAGTGA	2858
ATGGCGTCCC TTATCACCG CTAATGACTC TGACATCTCT CTCCACTCAC ATGTGAGCCT	2918
CCTCAGCTCT CGATAAACAA GTCTGTCTCG GTTCATTTAT TCTACAAAAA AAAAAAAAAA	2978
AAA	2981

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AATTCGGCAC GAGCAGCTTT CTAGTTGGAT TAGGCAACAG AATCCTTTGA AAATGTGTGT	60
GCACAGACCA GGTGGCTCTC TGGGCCAGTG TACTCTGAAA GATGTGTGTC CTGGCCTAGC	120
TGGTTGAGGA AAAGCAGGGC AAGCCTAGCC AAATCACACA TCTTGAACAG CCCTCATTCG	180
TTATACTAAC TTCCACCT TCTGGTGTGT ATAGGAGATA AAGATGGCAG ACGTGCTATT	240
AGGCTGCCAA TGGGAGTGGG CTCTGATATG GTCTTTCAAA T ATG AAT CAC CCC TGG	296

	Met	Asn	His	Pro	Trp	
	1				5	
CAT GTG TGT TTC CTG TTT AAG GTT CTC AGG TAT TAC CCA ACT GCA CCA						344
His Val Cys Phe Leu Phe Lys Val Leu Arg Tyr Tyr Pro Thr Ala Pro						
	10			15	20	
ATA TTA AAA TGG ACA CAT ACC GTG TCA TGC AGT TGG TGC CGA AGT GTT						392
Ile Leu Lys Trp Thr His Thr Val Ser Cys Ser Trp Cys Arg Ser Val						
	25			30	35	
TTA AGG GAA GTT GTA GGC AAT GTG AGT TTA TCA GAA AAC TTC ACC ATA						440
Leu Arg Glu Val Val Gly Asn Val Ser Leu Ser Glu Asn Phe Thr Ile						
	40			45	50	
TCA GCA TTT TGC CCT GAG CTT ACA CCA TTC CCA GAT CAA GGT ACA AGC						488
Ser Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro Asp Gln Gly Thr Ser						
	55			60	65	
ACA ATG ATT TCC TTT CTT GAA AAG TTC AAC AAA AGC AAG AGA GAG ACA						536
Thr Met Ile Ser Phe Leu Glu Lys Phe Asn Lys Ser Lys Arg Glu Arg						
	70			75	80	85
TTG GAG TTG ATG CTG CAT TTT TAT TCT GTG TTA AGT CTT GAA CCT GCT						584
Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu Ser Leu Glu Pro Ala						
	90			95	100	
GTT GCT GAA CAT TGG TCA GGG GAA TTT GAG AAG TGG AAA GTG GGC TTT						632
Val Ala Glu His Trp Ser Gly Glu Phe Glu Lys Trp Lys Val Gly Phe						
	105			110	115	
TTT CAC CCT TTG AAA AGA GAG GAT GGA TTC TTC ACC AGA ACT GAC ATT						680
Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe Thr Arg Thr Asp Ile						
	120			125	130	
TAAAAAAGT CAGCGTGGCA CGTTTTAGTA TGTGTGGCAG ATCTAAASAG ACAATATTTT						740
GATCTCAGGA GTGTTTATTC TTGAACCATT TTCAGAACTC TAAGATTTGA GAAATAATAA						800
AATATTGACC ATCCTTCAAA GAGAAAAACA CAGGGCGATC TTTGGCATAG CCTGTCATTT						860
TGCTCACATT TCACTTCTCT CTCTCCAACT TCAGAGCCCC TGCTGTGGAA CAGGTGCTGT						920
GCTGGGTGGC AGGGGAGGTC TCTGGCTTTT TTTTTTTTTG ATCTCCGTCT TAACATCTAG						980
CCTACTGGAG GAAGTGATT TAATCATCCA CTTATCTGTT AACAATTATC TCTGAGGGCC						1040
CGTCACATTC AGAGAAGATT CTAGGTTCTC TACAAGTATC CTCTCACTGT GTACATACTA						1100
AATCAACATC CTGCTGGATT TCCCCAGAC ATCTCCCTTC ATCACCATTG GAGAGTATCC						1160
TCTAATTGCC AGCCCTATTC ACCATACTCA TCTCATTTGA TCTGGAGTTT TCTGAGAGTG						1220
ACCGGGGGTG GGATGGACAG GATAATTTAG CAAGAGTGTA TAAGTAAAT CTATATAATA						1280
AAAGTTATCT CCCTGTGCCC CCCATGATCT ATTCTTTATG TAGCAGTCTG AATGAGATTT						1340
TCAGAAACAA GAACCACTTT ACCTTAGTCT CTTCTTCTTC TTCTTCTTCT TTTCTTTTCT						1400
TTTTTTTATG TATTATGGGC AACAGAGCAA GACCCAGTCT CAGGAAAAAA AAAAAAAA						1460
A						1461

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCAAAGTGCT GGGATTATAG GCATGAGCCA CTGCGCCCGG CCAGAATACC CTATCCTTAA	60
ACATGAATTT AGGGGAGGGG AGGACACAAT TCAATCTATA ACAACTATCA CTGGCTGATT	120
TTGGCAGAGG CCTGTGCCT CCAGTATTTT GAGGGAGCTG AGGGCCACTG ATCTCTCCAT	180

ATGCTCTCAA	CATCATGGGA	CTAGTAGGAT	GAAAGCAAGC	CTCAGACCAG	ATTCTACCTC	240
AAGCAGGCAC	ACAAACATTC	ATGCAGCTTC	TACTTGGAGC	CTGATGAAGT	TCAAATTGTT	300
TGTCTCTGA	GGCTCTCTTT	GCATGGAAAT	TTCTCCCATG	ACAGATGAGA	AAGTTCTGGG	360
GCAGCATTCA	GCTTTCTAGT	TGGATTAGGC	AACAGAATCC	TTTGAAAATG	TCTGTGCACA	420
GACCAGGTGG	CTCTCTGGGC	CAGTGTACTC	TGAAAGATGT	GTGTCCTGGC	CTAGCTGGTT	480
GAGGAAAAGC	AGGGCAAGCC	TAGCCAAATC	ACACATCTTG	AACAGCCCTC	ATTGCTTATA	540
CTAACTTTCC	CACCCTCTGG	TGTGTATAGG	AGATAAAGAT	GGCAGACGTG	CTATTAGGCT	600
GCCAATGGGA	GTGGGCTCTG	ATATGGTCTT	TCAAAT ATG	AAT CAC CCC TGG CAT		654
			Met	Asn His Pro Trp His		
			1	5		
GTG TGT TTC CTG TTT AAG GTT CTC AGG TAT TAC	CCA ACT GCA CCA ATA	702				
Val Cys Phe Leu Phe Lys Val Leu Arg Tyr Tyr	Pro Thr Ala Pro Ile					
	10 15 20					
TTA AAA TGG ACA CAT ACC GTG TCA TGC AGT TGG TGC CGA AGT GTT TTA	750					
Leu Lys Trp Thr His Thr Val Ser Cys Ser Trp Cys Arg Ser Val Leu						
	25 30 35					
AGG GAA GTT GTA GGC AAT GTG AGT TTA TCA GAA AAC TTC ACC ATA TCA	798					
Arg Glu Val Val Gly Asn Val Ser Leu Ser Glu Asn Phe Thr Ile Ser						
	40 45 50					
GCA TTT TGC CCT GAG CTT ACA CCA TTC CCA GAT CAA GGT ACA AGC ACA	846					
Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro Asp Gln Gly Thr Ser Thr						
	55 60 65 70					
ATG ATT TCC TTT CTT GAA AAG TTC AAC AAA AGC AAG AGA GAG AGA TTG	894					
Met Ile Ser Phe Leu Glu Lys Phe Asn Lys Ser Lys Arg Glu Arg Leu						
	75 80 85					
GAG TTG ATG CTG CAT TTT TAT TCT GTG TTA AGT CTT GAA CCT GCT TTT	942					
Glu Leu Met Leu His Phe Tyr Ser Val Leu Ser Leu Glu Pro Ala Phe						
	90 95 100					
GCT GAA CAT TGG TCA GGG GAA TTT GAG AAG TGG AAA GTG GGC TTT TTT	990					
Ala Glu His Trp Ser Gly Glu Phe Glu Lys Trp Lys Val Gly Phe Phe						
	105 110 115					
CAC CCT TTG AAA AGA GAG GAT GGA TTC TTC ACC AGA ACT GAC ATT TAAAAA	1041					
His Pro Leu Lys Arg Glu Asp Gly Phe Phe Thr Arg Thr Asp Ile						
	120 125 130					
AAGTCAGCGT GGCACGTTTT AGTATGTGTG GCAGATCTAA AGAGACAATA TTTTGATCTC	1101					
AGGAGTGTTT ATTCTTGAAC CATTTTCAGA ACTCTAAGAT TTGAGAAAATA ATAAAAATATT	1161					
GACCATCCTT CAAAGAGAAA AACACAGGGC GATCTTTGGC ATAGCCTGTC ATTTTGCTCA	1221					
CATTTCACTT CTCTCTCTCC AACTTCAGAG CCCCTGCTGT GGAACAGGTG CTGTGCTGGG	1281					
TGGCAGGGGA GGTCTCTGGC TTTTTTTTTT TGATCTCCGT CTTAACATCT AGCCTACTGG	1341					
AGGAAGTGTA TTTAATCATC CACTTATCTG TTAACAATTA TCTCTGAGGG CCCGTCACAT	1401					
TCAGAGAAGA TTCTAGGTTT TCTACAAGTA TCCTCTCACT GTGTACATAC TAAATCAACA	1461					
TCCTGCTGGA TTTCCCCCAG ACATCTCCCT TCATCACCAT TGGAGAGTAT CCTCTAATTG	1521					
CCAGCCCTAT TCACCATACT CATCTCATTT GATCTGGAGT TTTCTGAGAG TGACCGGGGG	1581					
TGGGATGGAC AGGATAATTT AGCAAGAGTG TATAAGTAAA ATCTATATAA TAAAAGTTAT	1641					
CTCCCTGTGC CCCCCATGAT CTATTCTTTA TGTAGCAGTC TGAATGAGAT TTTCAGAAAC	1701					
AAGAACCACT TTACCTTAGT CTCTTCTTCT TCTTCTTCTT CTTTCTTTT CTTTTTTTTT	1761					
AGTATTATGG GGATCTGTTT CTGTTGCCCA GGGTGGAGTG CAGTGGTATG ATCTTGCTC	1821					
ACAGCAGCCT TGAACCTCCG GGCTCAAGTG GTCCTCCTGC CTCTGCTTCC CTAGTAGCTA	1881					
GGACTGCAGG TTTGTGCCAC CACACCTGGC TAATTGAAAA AAGAAATTTT TTTTCAATAG	1941					
AGACAGTGTC TTGCTATGTC CCCAGGCTGG TCTCAAACCTC CTGGCCTCAA GTGATCCTCC	2001					
TGTCTCATCC TCCCAAAGTG TTGGAATTAC AGGTGTGAGC TACTATACTC GGCCAGTACC	2061					
CTTCTCAAAA CACTTCAGCA CTTCCCATG CACTTGGGTT GAAATTCCCA CCACTCACTG	2121					
GGGCCCCAAA GACTCTTCAA GACTGAATCC TTGCTCAACA TTGTGACCTG CCCCCTACCA	2181					
CCTGCAGCCT CACTTGCTGT GCTCCAGCCA TGTGGATCTT CCTCCTGTCT CTAATACTGC	2241					
CTCAGGTCAT TTGCACCTGC TGTCTTCCC AAAGGCTGTG TGATTTCAT CAGTCAGTCT	2301					

TAGCTCGTAT	ACCTCCTTGG	AGACACCTCT	TCTGACCAAC	CAGTCCAAAG	AATCTCCTCT	2361
TATCATGTCA	CTCTGTTTTA	TTTATTTATT	TAGAGATGGA	GTCTCGCTCT	GTCAACCAGG	2421
CTGGAGTGCA	GTGGCGCGAT	CTCTGCTCAC	TGCAAGCTCC	ACCTCCTGGG	TTCATGCCGT	2481
TCTCCTGCCCT	CAGCCTCCTG	AGTAACTGGG	ACTATGGGCA	CCCACCACTA	CACCCGGCTA	2541
ATTTTTTGTA	TTTTTAGTGG	GGATGGGGTT	TCACTGTGTT	AGCCAGGATG	GTCTTGATCT	2601
CCTGACCTTG	TGATCTGCCT	GCCTCCACCT	CCCAAAGTGT	TTTATTTATT	TTAAAGGCAT	2661
GTATCACTCT	CTGAAAATTA	GCTTCTTTCT	TCTTTTTCCT	TGTTATCATC	CATTTCCCCG	2721
AACCAGAATA	GAAGTTCCTG	AGGCCAGAAC	TTCTGTCTCT	CTGCCCCTCA	CTATGTGTCT	2781
CTGGCACATA	CCCCAGTGCC	TGCCTGCTCT	AAAGTAAAT	CTAGTAAAT	ATTACTGTTG	2841
ACTAAATAAA	TGAATAAATC	CCTTTTAATG	CCCCTTTGGA	AGTTGCCAAG	TAAAGAATAG	2901
GATCCCTTTT	TAAGATTACA	CTTTTGGCTA	TTGATCTGTG	TGCTGGAAC	AAGATACAGT	2961
TTGAAGATAC	TACCATGGGA	CATGACATCA	GTTGAGCTGA	TTAAGGTTTT	AGTAATAAGA	3021
ATCCAGGATG	TGTCCGGGTG	CGGTGCTCAC	GCCTGTAATC	CTAGCATTTT	GGGAGACCGA	3081
GGCGGGCAGA	TCACGAGGTC	AGCAGTTTGA	GACCAGCCTG	ACCAACATGG	TGAAACCCCG	3141
TCTCTACTAA	AAAATACAGA	AATTAGCCGG	GTGTGGTGGT	GTCCACCTGT	AGTCCTAGCT	3201
ACTCAGGAGG	CTGGGGCAGG	AGAATTCTT	GAACCCGGGA	GGCGGAGGTT	GCAGTGAGCC	3261
GAGATCACAC	CAGTGCACTC	CAGCCTGGGC	AACAGAGCAA	GACCCAGTCT	CAGGAAAAAA	3321
AAAAAAA						3329

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTGAAGTGGG	AGTCAGGTGG	TTGACTGTG	CCTGGCTGCA	GTAGCAGCGG	CATCTCCCTT	60
GCACAGTTCT	CCTCCTCGGC	CTGCCCAAGA	GTCCACCAGG	CC ATG GAC GCA GTG		114
				Met Asp Ala Val		
				1		
GCT GTG TAT CAT GGC AAA ATC AGC AGG GAA ACC GGC GAG AAG CTC CTG						162
Ala Val Tyr His Gly Lys Ile Ser Arg Glu Thr Gly Glu Lys Leu Leu						
5 10 15 20						
CTT GCC ACT GGG CTG GAT GGC AGC TAT TTG CTG AGG GAC AGC GAG AGC						210
Leu Ala Thr Gly Leu Asp Gly Ser Tyr Leu Leu Arg Asp Ser Glu Ser						
25 30 35						
GTG CCA GGC GTG TAC TGC CTA TGT GTG CTG TAT CAC GGT TAC ATT TAT						258
Val Pro Gly Val Tyr Cys Leu Cys Val Leu Tyr His Gly Tyr Ile Tyr						
40 45 50						
ACA TAC CGA GTG TCC CAG ACA GAA ACA GGT TCT TGG AGT GCT GAG ACA						306
Thr Tyr Arg Val Ser Gln Thr Glu Thr Gly Ser Trp Ser Ala Glu Thr						
55 60 65						
GCA CCT GGG GTA CAT AAA AGA TAT TTC CGG AAA ATA AAA AAT CTC ATT						354
Ala Pro Gly Val His Lys Arg Tyr Phe Arg Lys Ile Lys Asn Leu Ile						
70 75 80						
TCA GCA TTT CAG AAG CCA GAT CAA GGC ATT GTA ATA CCT CTG CAG TAT						402
Ser Ala Phe Gln Lys Pro Asp Gln Gly Ile Val Ile Pro Leu Gln Tyr						
85 90 95 100						
CCA GTT GAG AAG AAG TCC TCA GCT AGA AGT ACA CAA GGT ACT ACA GGG						450
Pro Val Glu Lys Lys Ser Ser Ala Arg Ser Thr Gln Gly Thr Thr Gly						
105 110 115						

ATA AGA GAA GAT CCT GAT GTC TGC CTG AAA GCC CCA TGAAGAAAAA	496
Ile Arg Glu Asp Pro Asp Val Cys Leu Lys Ala Pro	
120	125
TAAAACACCT TGTACTTTAT TTTCTATAAT TTAAATATAT GCTAAGTCTT ATATATTGTA	556
GATAATACAG TTCGGTGAGC TACAAATGCA TTTCTAAGC CATTGTAGTC CTGTAATGGA	616
AGCATCTAGC ATGTCGTCAA AGCTGAAATG GACTTTTGTA CATAGTGAGG AGCTTTGAAA	676
CGAGGATTGG GAAAAGTAAT TCCGTAGGTT ATTTTCAGTT ATTATATTTA CAAATGGGAA	736
ACAAAAGGAT AATGAATACT TTATAAAGGA TTAATGTCAA TTCTTGCCAA ATATAAATAA	796
AAATAATCCT CAGTTTTTGT GAAAAGCTCC ATTTTGTAGT AAATATTATT TTATAGCTAC	856
TAATTTTAAA ATGCTCTGCT TGATTGTATG GTGGGAAGTT GGCTGGTGTC CCTTGTCTTT	916
GCCAAGTTCT CCACTAGCTA TGGTGTCTA GGCTCTTTT GGATTTTGA AGCTGTATAC	976
TGTGTGCTAA AACAAAGCACT AAACAAAGAG TGAAGGATTT ATGTTTAATT CTGAAAGCAA	1036
CCTTCTTGCC TAGTGTTCTG ATATTGGACA GTAAAATCCA CAGACCAACC TGGAGTTGAA	1096
AATCTTATAA TTTAAAATAT GCTCTAAACA TGTTTATCGT ATTTGATGCT ACAGGATTTG	1156
AAATTGTATT ACAAATCCAA TGAAATGAGT TTTTCTTTTC ATTTACCTCT GCCCCAGTTG	1216
TTTCTACTAC ATGGAAGACC TCATTTTGAA GGGAAATTC AGCAGCTGCA GCTCATGAGT	1276
AACTGATTTG TAACAAGCCT CCTTTTAAAG TAACCCTACA AAACCACTGG AAAGTTTATG	1336
GTTGTATTAT TTTTAAAAA AATTCCAAGT GATTGAACT TACACGAGAT ACAGAATTTT	1396
ATGCGGCATT TTCTTCTCAC ATTTATATTT TTGTGATTTT GTGATTGATT ATATGTCACT	1456
TTGCTACAGG GCTCACAGAA TTCATTCACT CAACAAACAT AATAGGGCGC TGAGGGCATA	1516
GAAGTAAAAA CACCTGGTCC CTGCTCTCAG TTCACTGTCT TGTGAGACGA GAAAACATA	1576
ACGATAAAAG ACAGTGAAAG AAAATAACGA TAAAAGACAG TGAAAGAAAA TAACAATAAA	1636
AGACAAGGAA AAAATAACAA TGAAAGTTGA TAAGTACATG ATAAGCGAGG TTCCCCGTGT	1696
GTAGGTAGAT CTGGTCTTTA GAGGCAGATA GATAGGTCAG TGCAAATACT CTGGTCCATG	1756
GGCCATATGA AAAGGCTAAG CTTCACTGTA AAATAATAAC TGGGAATTCT GGGTTGTGTA	1816
TGGGTGTGTTG TGAACCTGGT TTTAATTAGT GAACTGCTGA GAGACAGAGC TATCTCCAT	1876
GTACTGGCAA GACCTGATTT CTGAGCATTT AATATGGATG CCGTGGGAGT ACAAAGTGG	1936
AGTGTGGCCT GAGTAATGCA TTATGGGTGG TTTACCATT CTGAGGTAA AAGCATCACA	1996
TGAACCTGTA AAGGAATTTA AAAATCCTAC TTTCATAATA AGTTGCATAG GTTTAATAAT	2056
TTTTAATTAT ATGGCTTGAG TTTAAATTGT AATAGGCGTA ACTAATTTTA ACTCTATAAT	2116
GTGTTTATTC TGAATAATC CTAAACATAT GAATTATGTT TGCATGTTCA CTTCCAAGAG	2176
CCTTTTTTTT AAAAAAAGCT TTTTTTGAAT CATCAAGTCT TTCACATTTA AATAAAGTGT	2236
TTGAAAGCTT TATTTAAAAA AAAAAAAAAA AAAAAAAAAA	2276

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CACTTATAAA ATGTTAGGGC TTAATATTAT TCATAGATCG AGGATAGTTT CATTCTTAGT	60
CGCCTCCTTA GTCACCTCTC CTATACCAAT CTGAGACCAT TTTACAATTT AGAAAAGACA	120
AATAACTGGT TGGGTTACTT GATAGTATAA TAACC	155

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
GAAGGAGAAT ATGAAGAGGT TAGAAAAGNT CNGGNTTCTG TTGGTGAAAT GAAGGATGAA 60
GGGGAAGAGA CATTAAATTA TCCTGATACT ACCATTGACT TGTCTCACCT TCAACCCCAA 120
AGGTCCATCC AGAAATTGGC TTCAAAAGAG GAATCTTCTA ATTCTAGTGA CAGTAAATCA 180
CAGAGCCGGA GACATTTGTC AGCCAAGGAA AGAAGGGAAA TGAAAAAGAA AAAACTTCCA 240
AGTGACTCAG GAGATTTAGA AGCGTTAGAG GGAAAGGA 278
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
TTCTGACAAT GAGTAAGAAG AAAGAGGGTC TTGCCCTTTG GTTATTAAGA TTTATCATAG 60
AGCAATAATA ASTAAATCGG TGTATACCA GCACAGAGAT TAGACAAATA AACCAAGGGA 120
CTGGACTAAA TAAGC 135
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
ATGGTACCCA GTTTCAAATT AACATGGGTA TTTTACTTGT GTTCCCAAAT TTAACATTAG 60
GGAATTTTTG GTTGTGGGTC TGTATCACT AGAAAAATAT ATATATTGGT GCTGAAGATA 120
ATTTTGAGAT AATTAGACAA GACAGTTTAG CATTTACAAG AACAAGTTTG GCAGTTGAAG 180
AATCTATTTA TATGACT 197
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
CCACCGCACC TGGCTGATGC TTTTCTATCT GACTTCTTTC AGAGGACCCT GAAAGACACT 60
AAGTGGAATC TTTCTTGAA GTCTTCCAAG CTAAAACAAT TCTCTGGAAA GATCACCTCT 120
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
CGTTTACAGA TTCTCTTGGC GCTGGCGGTG GAACTACAAA GGGATCGGTG CCTATATCAC   60
AATACCAAAC TTGATAATAA TCTAGATTCT GTGTYTCTGC TTATAGACCA TGTTTGTAGT  120
AGGTAAGAGG AAAACTTCCT ATATTCTGAA ACAGCCTAAC ATTTTACAAA ATTTTAGTTT  180
TCTTTTTTTAG AGTCTTATCC TGTAGCTATA TAACAGTTCA TGTCTGATT AGCATTTGTT  240
CACGAGTAAA GCTGGAATA TGAAAATTGA AAAT                                274
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
GATTAGGTGA CCTTCCTTGA ARAGCCACGG GTTCCCATTA TCGAAATGCT ATTCATTACC   60
CGAGTCACCT ANGTTCTTAC AAAGGAAGCG AGAAAATTGC TTTGTTGGG CCATGCCCCT  120
TTTGCANAGG TTCCTAAGTA TAGTCGCCAN AATTTTTTTA ATGGCCTAAA G              171
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
AGGGGCGCTT GTTCTGCTCT CAGCAGATTG GTTACACGCG TCAGGTGGTG GCGATGACTT   60
AATTCCTAGC CCAAGAAGAA TATAATGTTA AAAGTGGTTA TGTAATTTT GTGCCTCTCC  120
TTTTTAATGC AGTATTTAGT TCAGATGTTG GCGATTTTTC A                      161
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
TATAAGGWGG GAACCTTACT ATCTCTAATG ACCTTACTGA TGCTGACTTT AATACTCTGT 60
GAAGGTTAGA GTTCAGTGAA TGTACCTAG AAACAGCCCC GGCTGTGGAA TACTTTATTC 120
TTAGCCCTAT ATTTGGGGTT TGGATGTCCA CTGTGCTGGT TCCCAGAGAT AGTAAGGGGA 180
TGAGAGTATT GGTTACATCT CCTGACCCAC ATACTTAAGA TCCAGATGAA CAAGACAGTT 240
TTCACCTCTG CTTGGTAGAA CCTATTTGYK SHAGGAAACA GYTCTAAAG AATGGTTCTA 300
GCCAGACCCT GTCGYTACCA GAA 323
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
AGTATGACAA ATAGTTTCTG CCTGATTGGT GAGATTGCGG ATGGGCCCCC ACTTTGTTTC 60
TCTTTCTGCA TAAAAATTTC AACATTTTTC CAAAATTTTC AAAAATTCTT CCTCAGTCTG 120
TACATCTTTG TTAATCAG 138
```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
TGATCCCCAC AATTTCTTGT GATTGGTGAG GAACTATAAA TGAATCCCAT CCAAGCTTAT 60
ACCAGAAAAA AGGAGCACAT TTTCTACAAA TTATATCATT TTAATCCAT TACCACATTA 120
TTTAGGGGA ACTAC 135
```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
CTGAGAGGAG CCATGTATAC AAACCACTTT TTCTAACATG GTCTTTATTA AACTTTGAAT 60
ATAAGTACAC CTGCTCGAAG TGTTCATCTA TATTATTTAA GAACAAGCAA CTGTAAACA 120
```

GTAAAATCAC AAAAGGTAAG TTGTTGGAAG ACAACAAAAA AGAATTACTA TATCTGATCC 180
TGGCTGTTTA TTTTAGAATC TGTTAATAGG CCTACAGCT 219

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACAGTGAGTG TGGCTGAAAC CTAAGCTGAA GGAAGGGAGG AGCAGGCACT GCCATGAGGG 60
GTCCCTGGAC AGAAACTCTT CAGCAGGCCT TGAAGTTTAG TTCAGGGGCT ACATGGAATA 120
CCACTATTTA GCACACAGGT GTGATCTGAG GTGAGGGACT ACCTTTTCGA TCTTGTTTTT 180
CTCATTTATT T 191

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTGGAGGTGA AGGGAAGGAA AGAAAGGAAA AACTATCTAC CTGGCAGGAA AAGAGATAAG 60
CTCCCAAGAA CACCAAAGCA GATGATGAGT CTAGCTCTAC CCAGCCTTCC TCCCCACGAA 120
TCCAGATCAT AGTAAGAAAC TCTGGGCT 148

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCACCACCAG AAATGAACAA AAAGCATTTT ACCTAAAAAT ACACCAGCAA AATGTACTCA 60
GCTTCAATCA CAAATACGAC TGCTTAAAC CGCAGAAATT TCCTCAACAC TCAGCCTTTA 120
TCACTCAGCT GGATTTTTTC CTTCAACAAT CACTACTCCA AGCATTGGGG AACACAATT 180
TTAATCATAC TCCAGTCGTT TCACAATGCA TTCTAATAGC AGCGGGATCA GAACAGTACT 240
GCATTACTT GCCAACAGAA CAGACAGACC TGAAGTCAAG ACAACTGCAT TCTCTGTGAA 300
GTCTGT 306

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (G) CELL TYPE: leukocyte
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTAGCATTTT	GGCAGAACCA	TTGTTAATTA	AAGGGACTTY	TGGACCGCAA	CYTTAATGTA	60
CCAGATTATT	GAGCRGCCCA	ATGAATGCTT	CATTCTCATT	GTTTAAGGTG	CTGCTTTGAT	120
TTTTTTTTC	ATTCTTTGTA	CTATTTTTTA	TTTTTTGGAG	AGGCACATCC	CCAAATTGG	180
ATGAGGTATT	TGTTGATAAA	TAATTCATCA	ATTTCCACAA	TGCAGACAAA	AATGTCTGCC	240
CAGAGTGGAA	AAATAAAACA	AGGGGGAGAA	GAGTTTGAGT	AACGGAGAAG	TTCTGTGGAA	300
TCCTAGTGAC	AAAAGTTGAG	AACTACCTT	TAAATAAGAC	ACTGAGGTAA	CAAATGT	357

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 219 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (G) CELL TYPE: leukocyte
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGGAATAGCC	AGGAGAATTC	TGGAAGAGTA	GAATAATGAG	GTAGGGCTTC	CCTTCGCTAT	60
TTTGAAGTGC	AGATTACACT	ATGTAAAACC	ATTAGGAACT	GGCACGTGAA	TAGACGATC	120
AATAGTTAAT	AGCTGTATTA	GCCAGAAAAT	GGTGTAAAGGA	CAACAGGCTA	ACTAACCCTG	180
TCACTTGTTA	TGCTAAAATT	AAGTCTAGAT	AGAGTCCTC			219

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (G) CELL TYPE: leukocyte
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGAAAGGGGA	ATAGAAGCAC	AAGAGTCAGT	AATCAATAAC	AAACAACCTCA	AGGTGCTCCT	60
TCCTTACACT	GGTGTTCCCC	AAAGTGAGGT	GAATTGCCAG	CCACTGGGAG	TCAGGGCCAG	120
TTACATAAGA	CATTCTCGGT	AAGCCCCCTT	TGGGTATCCC	AAATAAGGAC	TGGGGTGGGT	180
TTATGTGTAG	TCCATTATTA	ACAACTAAAC	GAACAAACCT	ACTGAATTGC	AATAAATTCA	240
CACCAACAGA	A					251

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
GTTGAAAGAG TCCTTGAAG GCTTTTAGAC CAAACCCCTC TGCATGCTCA ARCCTTGGGT 60
ACAGGATTTT TAAGAAGTGG AACAGTCTCC AGGGGTGTGG ARCTCATCGC TCAAGGCAGG 120
TTATCTTATC TGAATAATTT TGTCTGTTGA CTATTGGGAT AGTTCTCCTT CAGATGAGCT 180
GAAATTTTCT CCATAGCTTC CTCTATTAAA CCCAATTCCA CTTCTCAGGG TCA 233
```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
CAAAGCGCT GAAGTTAAGC ATTAATACGC CAGATTCATG ATTTATGATC AGTATCCAAA 60
ACTCCAATA CAAACAATGC AAAGTAGTGC TCCTCAGTAT TATTTTTGCA ATTGTTAGTA 120
ATGTTAAGCA TCAAGGAAAA TAAAACACAT CATTGCACAT TACAGCCGCA AAAAAC 176
```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
AGAGAGTAAA GCAAGCTATT TTGACAGCAA CCTAATAACA GCTGTCTTCT TCCACTTCTT 60
GGCTAACTCA TCCCCCAGAT AGCCTTCTTT TCTCTTATCA ATTCCCTGTT GCAACAATAA 120
TAAATGCCAC ACCTGATGGA GTCATTAGGC ACTTTCCTAG TGACAAGTGC CTAGGACAGA 180
GGAGAAAACA AAGAAACACT GACAACCACT GAAAACTGAC ATATCAGGCC AGGCATGTCA 240
C 241
```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
GCTGGAGAGG TGGTGATGTT GCTGAATAAT TGCTTTTTTAA AGCTGGAGGG GACTTCCAAG 60
AGTCTCTCAT TTAAGAARAA AAATTAAAGA CATAATTGGT AACGGTTTTG ACTGCTGCAG 120
AGGCAACACT TTGCTCACAA TCCTACAGAT CTACTTCACC TGTAACATAA ATTTTCCTGA 180
```


(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
AATCTTAGCA TAATGCTTCC TGGGAAATTC TGAAATTGAT TCCATTTCTG CCGTTACAAA 60
CACACACGAA GTTCCTAGTT CACTGGGACT TCCTGATTG TTCTTTTAGC TTGCTCCTTC 120
TCACCTAGAA GCTCTGTTTA TTTCTGAGCA ACCCTGGGGC TTGTCTCATA GGACAGGATT 180
TATTTATCTC ATCAAGGCTG AGTGTGCCTT AGGAAGTCAT AACATAAAA AGA 233
```

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
TATAGACAGG GTAGGGACGA TTAGCCCCTC GACAACTTTT CACAAATATA CACACGTTTA 60
ACTACCTCTC AGGTCATGAT AAAGACCGGC CGGGCAGAAA CACTGTAATC CCAGCTACTC 120
GGGAGCCTGA GGCATGAGAA TCACTGAAC CTGGGAGGTG GAGGTTGCCA TGAGCCGAGA 180
TCACGCCATT GCACTACAGC CTTGGCGACA AGAGTGAAAC TCCATCTG 228
```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
GCTTATGATT ACAAACATCC CTCATATGAA AATCTCAGCA TTNCTGGCT GCTGCCTTCA 60
ATCGCTTTTT CTGAAATAGG TATCCCTTGA TGTCGACTAT TTGATTTAG CCAGTCGTTT 120
CTCTCTGGCA GTGCTCCCTG CAAATGTGTC CTTTCAAGAA AACAAAACCT GCAAGTGGCT 180
TGTAATGTAC CATGACCTTA TCATGTGAAG GACAAATGGC TCTGTGCTT ATTAGATAGC 240
AGATGAACTG ATGAACTGAA TTCTTGGTCT GAAGCTTTGA TAAGGTCAGA TGTCTTTG 298
```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(i) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
ACTTCGAAGG GAAAAAGAGG AAGGAAAAGG ACTGTTAATA AAATAACAAA GGCAGCAATC 60
AGAATGAACC AGAGCCAGGA CAGCGTAAAG GCTAGGTTCA CAGTGAGATG AAAGAACCTG 120
AAAACAAGTT TAAAACTCAA AAGAGGATTA TTCTCAAGTT ATACTACAGT GAAAAACAT 180
GGAAAAACAC AAAAAGGACA GGCAATAAGG CACAGGCATA CATACAAGGC AAATTGTAAC 240
ACAATATTTA CTTGCAAAAG AGCCACAGA GACATGTCAA TGAAGTCATA G 291
```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
Met Glu Asp Gly Phe Leu Asp Asp Gly Arg Gly Asp Gln Pro Leu His
 1           5           10           15
Ser Gly Leu Gly Ser Pro His Cys Phe Ser His Gln Asn Gly Glu Arg
 20           25           30
Val Glu Arg Tyr Ser Arg Lys Val Phe Val Gly Gly Leu Pro Pro Asp
 35           40           45
Ile Asp Glu Asp Glu Ile Thr Ala Ser Phe Arg Arg Phe Gly Pro Leu
 50           55           60
Ile Val Asp Trp Pro His Lys Ala Glu Ser Lys Ser Tyr Phe Pro Pro
 65           70           75           80
Lys Gly Tyr Ala Phe Leu Leu Phe Gln Asp Glu Ser Ser Val Gln Ala
 85           90           95
Leu Ile Asp Ala Cys Ile Glu Glu Asp Gly Lys Leu Tyr Leu Cys Val
100           105           110
Ser Ser Pro Thr Ile Lys Asp Lys Pro Val Gln Ile Arg Pro Trp Asn
115           120           125
Leu Ser Asp Ser Asp Phe Val Met Asp Gly Ser Gln Pro Leu Asp Pro
130           135           140
Arg Lys Thr Ile Phe Val Gly Gly Val Pro Arg Pro Leu Arg Ala Val
145           150           155           160
Glu Leu Ala Met Val Met Asp Arg Leu Tyr Gly Gly Val Cys Tyr Ala
165           170           175
Gly Ile Asp Thr Asp Pro Glu Leu Lys Tyr Pro Lys Gly Ala Gly Arg
180           185           190
Val Ala Phe Ser Asn Gln Gln Ser Tyr Ile Ala Ala Ile Ser Ala Arg
195           200           205
Phe Val Gln Leu Gln His Gly Glu Ile Asp Lys Arg Val Ser Leu Ile
210           215           220
Leu His Phe Gly Lys Phe
225           230
```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Gly	Ser	Asp	Lys	Arg	Val	Ser	Arg	Thr	Glu	Arg	Ser	Gly	Arg	Tyr
1				5					10					15	
Gly	Ser	Ile	Ile	Asp	Arg	Asp	Asp	Arg	Asp	Glu	Arg	Glu	Ser	Arg	Ser
			20					25					30		
Arg	Arg	Arg	Asp	Ser	Asp	Tyr	Lys	Arg	Ser	Ser	Asp	Asp	Arg	Arg	Gly
			35				40					45			
Asp	Arg	Tyr	Asp	Asp	Tyr	Arg	Asp	Tyr	Asp	Ser	Pro	Glu	Arg	Glu	Arg
		50				55				60					
Glu	Arg	Arg	Asn	Ser	Asp	Arg	Ser	Glu	Asp	Gly	Tyr	His	Ser	Asp	Gly
65					70					75				80	
Asp	Tyr	Gly	Glu	His	Asp	Tyr	Arg	His	Asp	Ile	Ser	Asp	Glu	Arg	Glu
				85					90					95	
Ser	Lys	Thr	Ile	Met	Leu	Arg	Gly	Leu	Pro	Ile	Thr	Ile	Thr	Glu	Ser
			100				105						110		
Asp	Ile	Arg	Glu	Met	Met	Glu	Ser	Phe	Glu	Gly	Pro	Gln	Pro	Ala	Asp
		115				120						125			
Val	Arg	Leu	Met	Lys	Arg	Lys	Thr	Gly	Glu	Ser	Leu	Leu	Ser	Ser	
		130				135					140			143	

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(B) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met	Pro	His	Met	Leu	Ser	Gln	Leu	Ile	Ala	Gly	Gly	Val	Ser	Thr	Ser
1				5					10					15	
Cys	Val	Thr	Ala	Leu	Gly	Glu	Glu	Thr	Gly	Ala	Trp	Phe	Pro	Val	Tyr
			20					25					30		
Leu	Ser	His	Ala	Ser	Ser	Pro	Phe	Ala	Asp	Leu	Val	Phe	Cys	Pro	Phe
			35				40					45			
Ala	Glu	Ile	Asn	His	Ser	Gln	Glu	Tyr	Asp	Asn	Met	Arg	Gly	Pro	Val
		50				55				60					
Ser	Pro	Pro	Asn	Lys	Gln	Phe	Asn	Leu	Gly	Val	Ile	Phe	Gly	Ile	Pro
65				70						75				80	
Asn	Asn	Cys	Arg	Phe	Pro	Thr	Asp	Asn	Lys	Ile	Thr	Glu	Lys	Gln	Leu
			85						90					95	
Leu	Gly	Asn	Val	Leu	Asn	Tyr	Pro								
			100												

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids
 (B) SEQUENCE TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (vi) ORIGINAL SOURCE:

(A) ORGANISM: human
 (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

Met Asn His Pro Trp His Val Cys Phe Leu Phe Lys Val Leu Arg Tyr
 1           5           10           15Pro Thr Ala
Pro Ile Leu Lys Trp Thr His Thr Val Ser Cys Ser
           20           25           30
Trp Cys Arg Ser Val Leu Arg Glu Val Val Gly Asn Val Ser Leu Ser
           35           40           45
Glu Asn Phe Thr Ile Ser Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro
           50           55           60
Asp Gln Gly Thr Ser Thr Met Ile Ser Phe Leu Glu Lys Phe Asn Lys
           65           70           75           80
Ser Lys Arg Glu Arg Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu
           85           90           95
Ser Leu Glu Pro Ala Val Ala Glu His Trp Ser Gly Glu Phe Glu Lys
           100          105          110
Trp Lys Val Gly Phe Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe
           115          120          125
Thr Arg Thr Asp Ile
           130
  
```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human
 (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

Met Asn His Pro Trp His Val Cys Phe Leu Phe Lys Val Leu Arg Tyr
 1           5           10           15
Tyr Pro Thr Ala Pro Ile Leu Lys Trp Thr His Thr Val Ser Cys Ser
           20           25           30
Trp Cys Arg Ser Val Leu Arg Glu Val Val Gly Asn Val Ser Leu Ser
           35           40           45
Glu Asn Phe Thr Ile Ser Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro
           50           55           60
Asp Gln Gly Thr Ser Thr Met Ile Ser Phe Leu Glu Lys Phe Asn Lys
           65           70           75           80
Ser Lys Arg Glu Arg Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu
           85           90           95
Ser Leu Glu Pro Ala Phe Ala Glu His Trp Ser Gly Glu Phe Glu Lys
           100          105          110
Trp Lys Val Gly Phe Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe
           115          120          125
Thr Arg Thr Asp Ile
           130
  
```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) SEQUENCE TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met	Asp	Ala	Val	Ala	Val	Tyr	His	Gly	Lys	Ile	Ser	Arg	Glu	Thr	Gly
1				5					10					15	
Glu	Lys	Leu	Leu	Leu	Ala	Thr	Gly	Leu	Asp	Gly	Ser	Tyr	Leu	Leu	Arg
			20					25					30		
Asp	Ser	Glu	Ser	Val	Pro	Gly	Val	Tyr	Cys	Leu	Cys	Val	Leu	Tyr	His
		35				40					45				
Gly	Tyr	Ile	Tyr	Thr	Tyr	Arg	Val	Ser	Gln	Thr	Glu	Thr	Gly	Ser	Trp
	50					55				60					
Ser	Ala	Glu	Thr	Ala	Pro	Gly	Val	His	Lys	Arg	Tyr	Phe	Arg	Lys	Ile
	65				70				75					80	
Lys	Asn	Leu	Ile	Ser	Ala	Phe	Gln	Lys	Pro	Asp	Gln	Gly	Ile	Val	Ile
			85					90					95		
Pro	Leu	Gln	Tyr	Pro	Val	Glu	Lys	Lys	Ser	Ser	Ala	Arg	Ser	Thr	Gln
		100					105					110			
Gly	Thr	Thr	Gly	Ile	Arg	Glu	Asp	Pro	Asp	Val	Cys	Leu	Lys	Ala	Pro
	115					120						125			

(2) INFORMATION FOR SEQ ID NO:39:

(i) LENGTH: 305 base pairs

- (A) TYPE: nucleic acid
- (B) STRANDEDNESS: double
- (C) TOPOLOGY: linear
- (D) MOLECULE TYPE: cDNA

(ii) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCATGAAGTG AAGCCAACTG TTAGACTAG AATGTTATGA GATTAAACCC ACNNNNNNNTT	60
ATTCATAGAC ATAAACCCTC ATTTTAATTA GTGGATCTGG ATTTTGTGCA TATGTGGAAT	120
CATAATTTAA ACAAATCAA CTAAGATGAT CCAAGTTCCA CAACTGCA CTTCAATATT	180
CAAGTCGGTG TGAAGATGCC TGA TACTGTC GTCACAAGAT TCTGAGCTGT CGTAAAAAGC	240
CTGGCTCGTG GTTCTATTT ATAGTGACA CATGTTGGGT TATAATCACA AACCTGGAAC	300
TCTGT	305

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAAACCACGG	CTTACACCTA	GAGACAGCAT	TCAGATATAG	ACGGGATACT	TGTGTTAGTC	60
AGTTCCTTTA	TAACAGGTGA	ATCTCTCTCC	CACTGCTTCA	ACACTGCGTG	ACAAAGCCAA	120
TTGGGAAGCA	GCTTTACAAA	TGTGACTTGA	CTTGGGGATC	TTCTTGATAC	TTTGCCATGG	180
CAAGGAACAA	GCCGCCTGAA	CTAAATGCCA	CTCCATTTGA	TTCCACGCTT	AAAGTAACCA	240
TGCAACCGAC	TATAGT					256

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TACTCTTCAA	CCATGATTTT	TCTCTGATGG	CCTGTGTGAA	CAGATTAATG	GTGTCCATCT	60
AATTCCTTCC	CCACTGGGGG	AAAGCAAATC	ATCAGGCCCA	TTGCAAAAAC	TGCTCTTGGT	120
TGAGCTTCCT	GCCTTAAATC	ATACCCACAG	TGAATGGCGT	CCCTTTATCA	CCGCTAATGA	180
CTCTGACATC	TCTCTCCACT	CACATGTGAG	CCTCCTCAGC	TCTCGANAAA	CAAGTCNGTC	240
TCGG						244

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (G) CELL TYPE: leukocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCTCAGAAAA	CTCCAGATCA	AATGAGATGA	GTATGGTGNN	NAGGGCTGGC	AATTAGAGGA	60
TACTCTCCAA	TGGTGATGAA	GGGAGATGTC	TGGGGGAAAT	CCAGCAGGAT	GTTGATTTAG	120
TATGTACACA	GTGAGAGGAT	ACTTGTAGAG	AACCTAGAAT	CTTCTCTGAA	TGTGACGGGC	180
CCTCAGAGAT	AATTGTTAAC	AGATAAGTGG	ATGATTAAAT	ACACTTCCTC	CAGTAGGCTA	240
GATGTTAAGA	CGGAGATC					258

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid; synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGGCTTAATA	TTATTCATAG	ATCGAG	26
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(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:
GTTATTATAC TATCAAGTAA CCCAAC 26

(2) INFORMATION FOR SEQ ID NO:45:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:
GTGGATCTGG ATTTTGTCA TATGT 25

(2) INFORMATION FOR SEQ ID NO:46:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
GTTTGTGATT ATAACCAAC ATGTG 25

(2) INFORMATION FOR SEQ ID NO:47:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:
GAAGGGGAAG AGACATTAAA TTATC 25

(2) INFORMATION FOR SEQ ID NO:48:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:
GCTTCTAAAT CTCCTGAGTC ACTT 24

(2) INFORMATION FOR SEQ ID NO:49:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:
GACAATGAGT AAGAAGAAAG AGGG 24

(2) INFORMATION FOR SEQ ID NO:50:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:
 GTCCAGTCCC TTGGTTTATT TGTC 24

(2) INFORMATION FOR SEQ ID NO:51:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:
 GGTACCCAGT TTCAAATTAA CATGG 25

(2) INFORMATION FOR SEQ ID NO:52:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:
 GATTCTTCAA CTGCCAAACT TGTTC 25

(2) INFORMATION FOR SEQ ID NO:53:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:
 GCTGATGCTT TTCTATCTGA CTTC 24

(2) INFORMATION FOR SEQ ID NO:54:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:
 GACCAGGACT GAACAGAGGT GA 22

(2) INFORMATION FOR SEQ ID NO:55:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
GCTTATAGAC CATGTTTGTA GTAGG 25

(2) INFORMATION FOR SEQ ID NO:56:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:
GTGAACAAAT GCTAAATCAG ACATG 25

(2) INFORMATION FOR SEQ ID NO:57:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:
GCCACGGGTT TCCCATATCG AA 22

(2) INFORMATION FOR SEQ ID NO:58:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:
GACTATACTT AGGAACCTCT GCAA 24

(2) INFORMATION FOR SEQ ID NO:59:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:
GTTCTGCTCT CAGCAGATTG GTTA 24

(2) INFORMATION FOR SEQ ID NO:60:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:
GCCACATCT GAACTAAATA CTGC 24

(2) INFORMATION FOR SEQ ID NO:61:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:
GTTTCAGTGAA TGTTACCTAG AAACA 25

(2) INFORMATION FOR SEQ ID NO:62:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:
GGAGTGAAAA CTGTCTTGTT CATC 24

(2) INFORMATION FOR SEQ ID NO:63:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:
GTATGACAAA TAGTTTCTGC CTGAT 25

(2) INFORMATION FOR SEQ ID NO:64:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:
GATTACAAA GATGTACAGA CTGAG 25

(2) INFORMATION FOR SEQ ID NO:65:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:
GAGACAGCAT TCAGATATAG ACGG 24

(2) INFORMATION FOR SEQ ID NO:66:
(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
GCGTGGAATC AAATGGAGTG GC 22

(2) INFORMATION FOR SEQ ID NO:67:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:
GATGGCCTGT GTGAACAGAT TAAT 24

(2) INFORMATION FOR SEQ ID NO:68:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:
GAGAGAGATG TCAGAGTCAT TAGC 24

(2) INFORMATION FOR SEQ ID NO:69:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
GATCCCCACA ATTTCTTGTG ATTG 24

(2) INFORMATION FOR SEQ ID NO:70:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:
GTTCCCCTAA AATAATGTGG TAATG 25

(2) INFORMATION FOR SEQ ID NO:71:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:
GAGGATACTC TCCAATGGTG ATG 23

(2) INFORMATION FOR SEQ ID NO:72:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:
GTCTTAACAT CTAGCCTACT GGAG 24

(2) INFORMATION FOR SEQ ID NO:73:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:
GAGAGGAGCC ATGTATACAA ACCA 24

(2) INFORMATION FOR SEQ ID NO:74:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:
GCACGCAGGA TCAGATATAG TAATTC 26

(2) INFORMATION FOR SEQ ID NO:75:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:
GCTGAAACCT AAGCTGAAGG AAGG 24

(2) INFORMATION FOR SEQ ID NO:76:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:
GTCCCTCACC TCAGATCACA CC 22

(2) INFORMATION FOR SEQ ID NO:77:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:
GCTATCTACC TGGCAGGAAA AGAG 24

(2) INFORMATION FOR SEQ ID NO:78:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:
GAGTTTCTTA CTATGATCTG GATTC 25

(2) INFORMATION FOR SEQ ID NO:79:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:
GCAAAATGTA CTCAGCTTCA ATCAC 25

(2) INFORMATION FOR SEQ ID NO:80:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:
GTAAATGCAG TACTGTTCTG ATCC 24

(2) INFORMATION FOR SEQ ID NO:81:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:
GAATGCTTCA TTCTCATTGT TTAAGG 26

(2) INFORMATION FOR SEQ ID NO:82:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:
GTCAC TAGGA TTCCACAGAA CTTC 24

(2) INFORMATION FOR SEQ ID NO:83:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:
GAGGTAGGGC TTCCCTTCGC TA 22

(2) INFORMATION FOR SEQ ID NO:84:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:
GCATAACAAG TGACAGGGTT ACTTA 25

(2) INFORMATION FOR SEQ ID NO:85:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:
GGTGCTCCTT CCTTACACTG GT 22

(2) INFORMATION FOR SEQ ID NO:86:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:
GACTACACAT AAACCCACCC CAG 23

(2) INFORMATION FOR SEQ ID NO:87:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:
GGGTACAGGA TTTCTAAGAA GTGG 24

(2) INFORMATION FOR SEQ ID NO:88:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:
 GGAGAAAATT TCAGTCATC TGAAG 25

(2) INFORMATION FOR SEQ ID NO:89:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:
 GCTGAAGTTA AGCATTAATA CGCC 24

(2) INFORMATION FOR SEQ ID NO:90:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:
 GCGGCTGTAA TGTGCAATGA TGT 23

(2) INFORMATION FOR SEQ ID NO:91:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:
 GACAGCAACC TAATAACAGC TGTC 24

(2) INFORMATION FOR SEQ ID NO:92:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:
 GTCCTAGGCA CTTGTCACTA GG 22

(2) INFORMATION FOR SEQ ID NO:93:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:
 GAGGGGACTT CCAAGAGTCT CT 22

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GTCTTCAGGA AAATTGTAGT TACAG

25

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GTTACAAACA CACACGAAGT TCCT

24

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GACTTCCTAA GGCACACTCA GC

22

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTTTAACTAC CTCTCAGGTC ATGA

24

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTCGCCAAGG CTGTAGTGCA AT

22

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:
GAAATAGGTA TCCCTTGATG TCGA 24

(2) INFORMATION FOR SEQ ID NO:100:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:
GACCAAGAAT TCAGTTCATC AGTT 24

(2) INFORMATION FOR SEQ ID NO:101:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:
GAATGAACCA GAGCCAGGAC AG 22

(2) INFORMATION FOR SEQ ID NO:102:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:
GCCTTGATG TATGCCTGTG CC 22

(2) INFORMATION FOR SEQ ID NO:103:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:
AAGAGTCCAC CAGGCCATGG A 21

(2) INFORMATION FOR SEQ ID NO:104:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:
TACCTTGTT ACTTCTAGCT GAG 23

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTTTTTTTTT TTTTTA

17

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GTTTTTTTTT TTTTGT

17

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GTTTTTTTTT TTTTTC

17

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CAGAGTGATG GATATCAA

18

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATGAAAGTGC CAGTGTGCCA TG

22

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:
CCCATCACCA TCTTCCAGGA GC

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(2) INFORMATION FOR SEQ ID NO:111:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:
TTCACCACCT TCTTGATGTC ATCATA

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